

Figure 1

A 1 2 3 4 5 6 7 8 9 10 11 12 13 14

197-

197-

197-

B 1 2 3 4 5 6 7 8 9 10 11 12 13 14

197-

197-

197-

Fraction: 28 30 32 34 36 38 40 42 81 83 85 87 89 91



105240" 0E624860

Figure 3

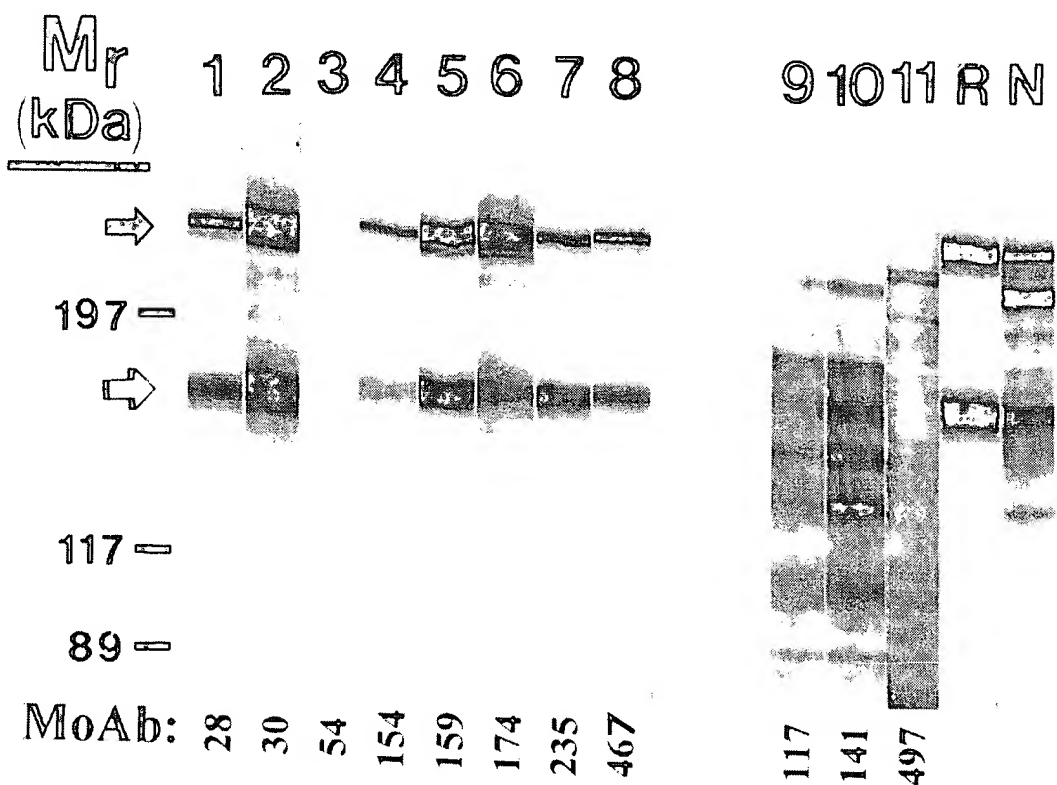
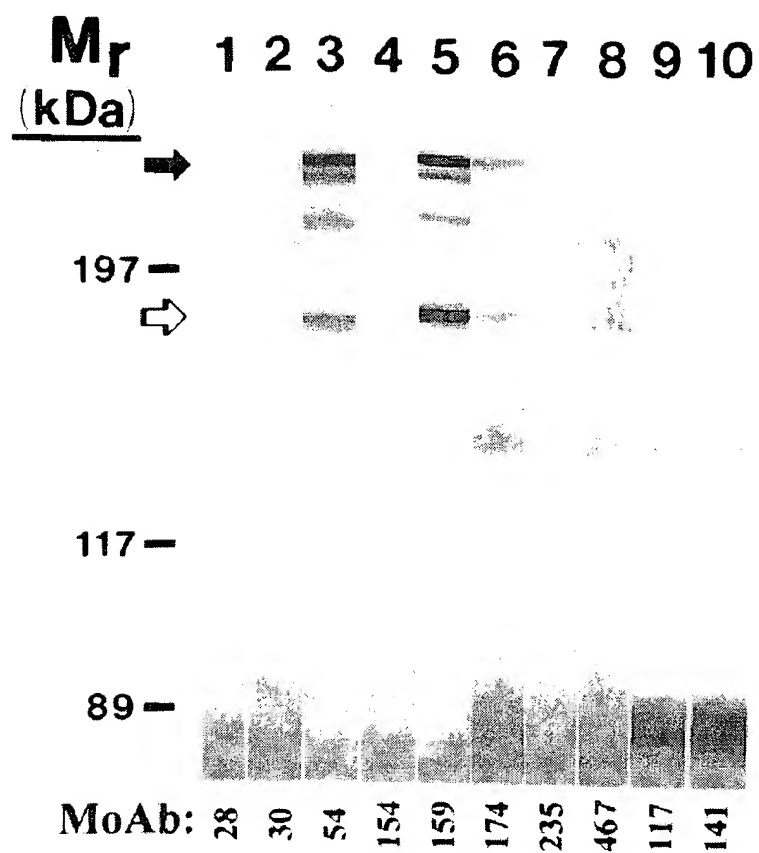


Figure 4



T05240-0E624860



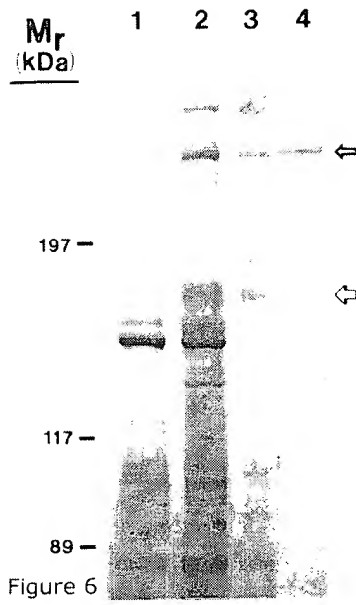


Figure 6

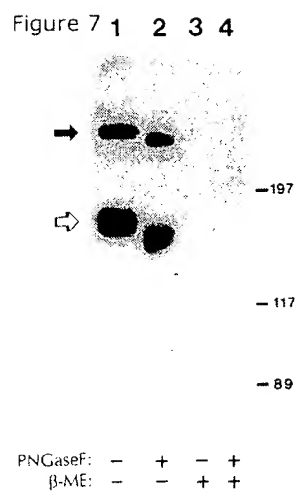


Figure 8A

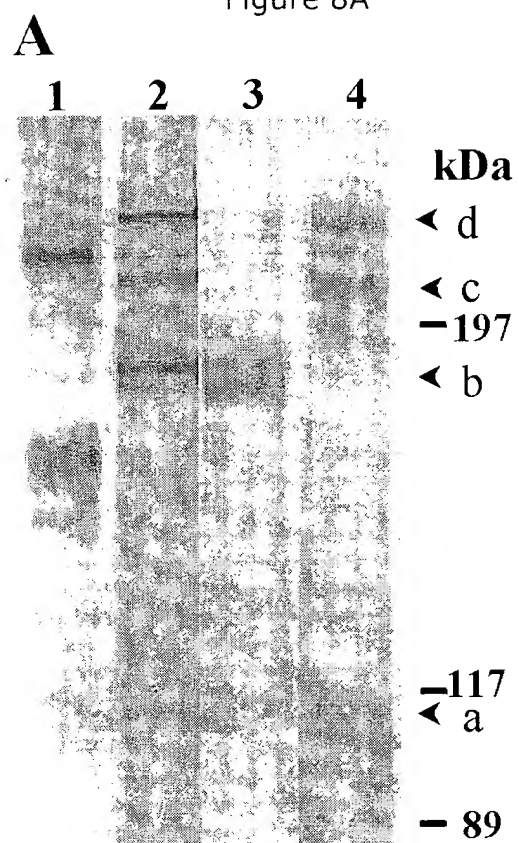
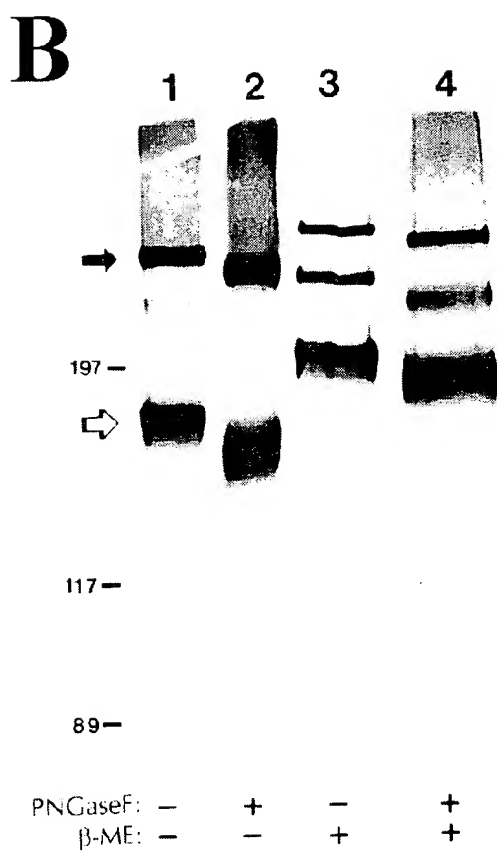
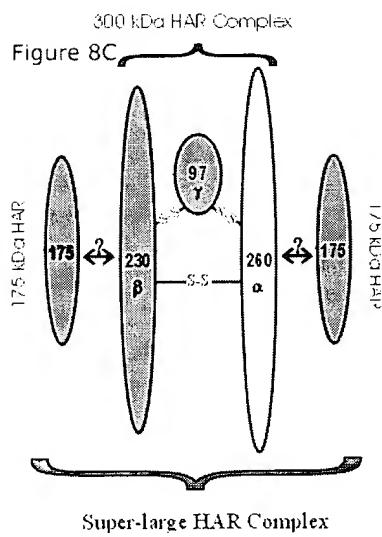




Figure 8B



094930-04501



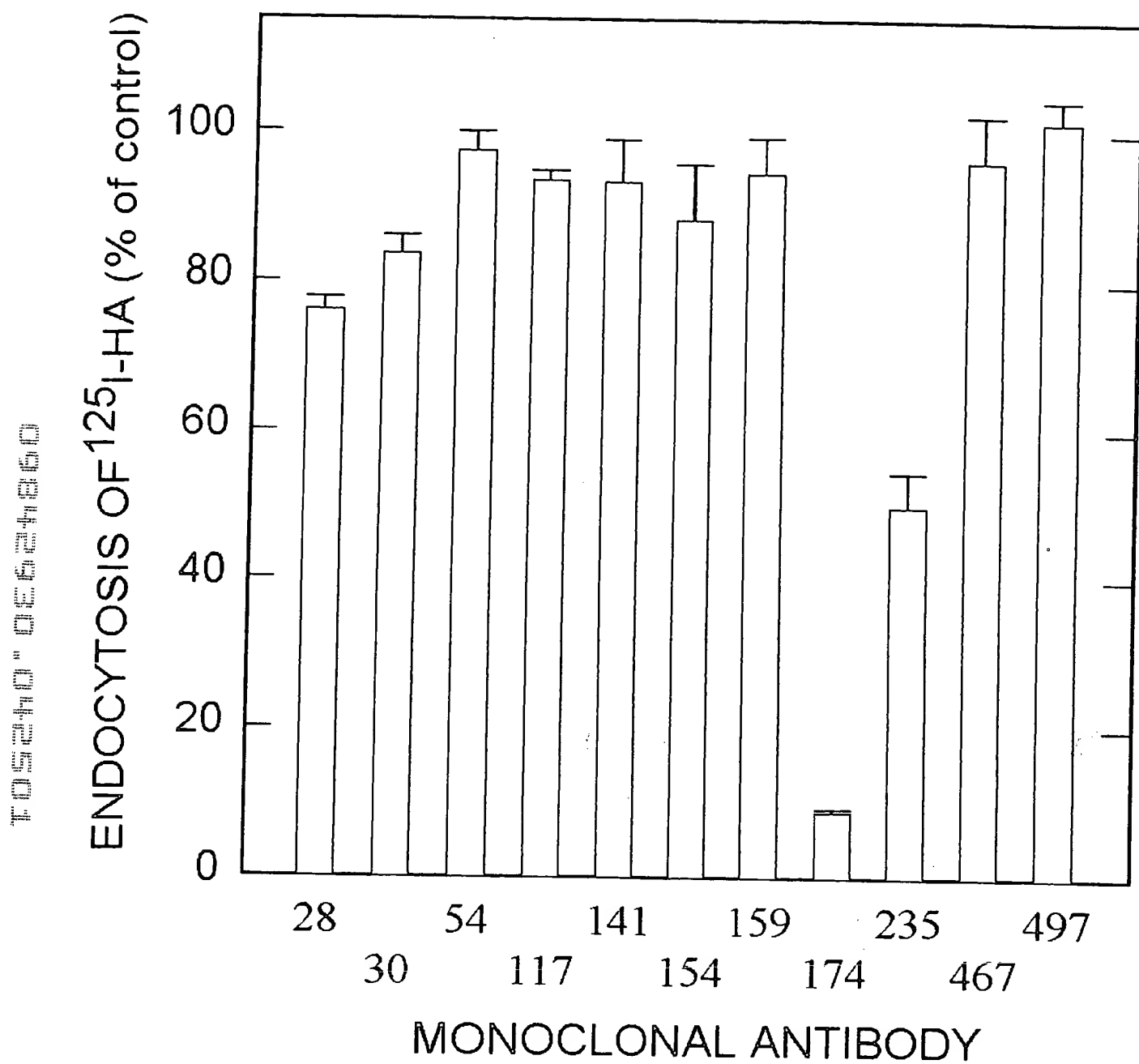
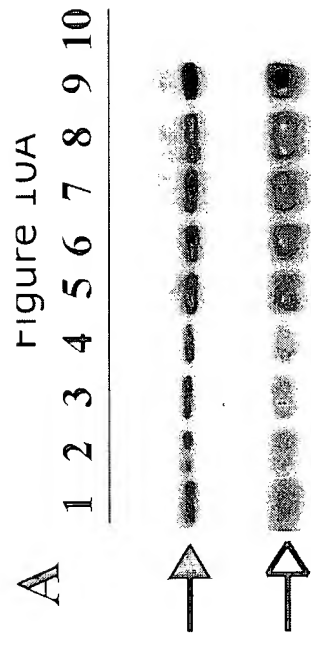


Figure 9



105240" 06624860

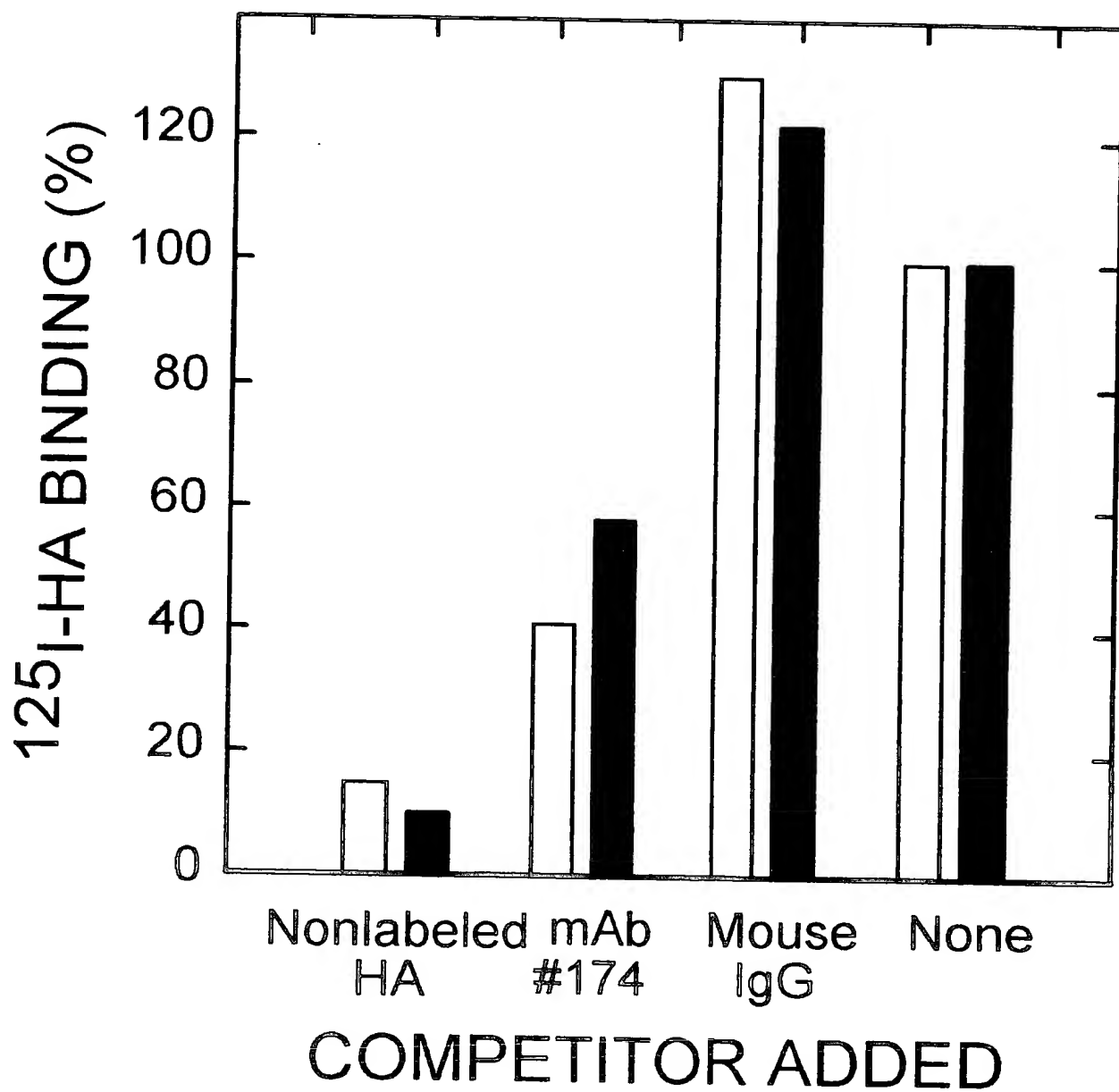


Figure 10B

Figure 11

Antibody Inhibition of HLA  
Endocytosis by HARE in LECs

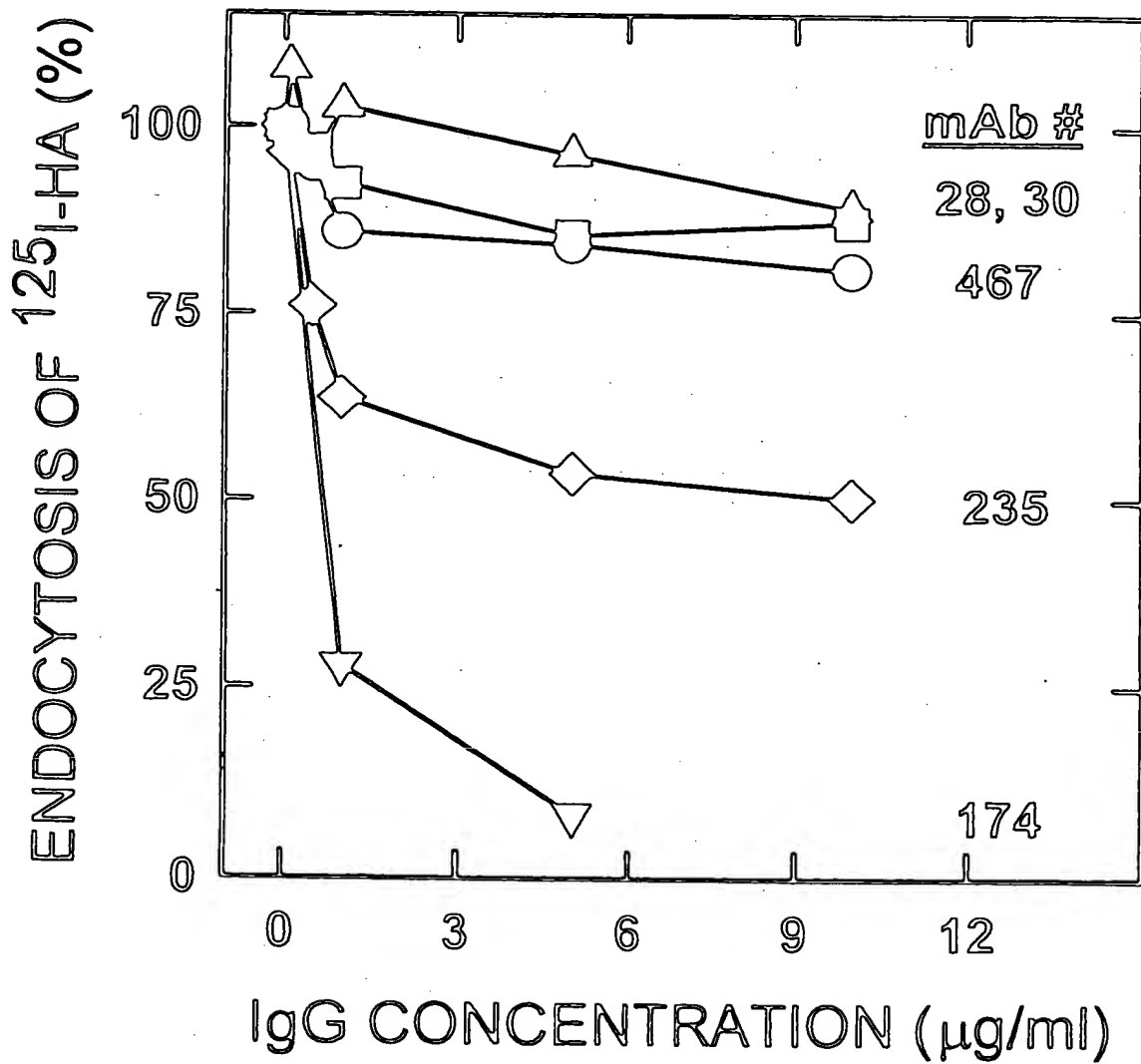


Figure 12

# Antibody Inhibition of HA Binding to HARE on LECs is Temperature Dependent

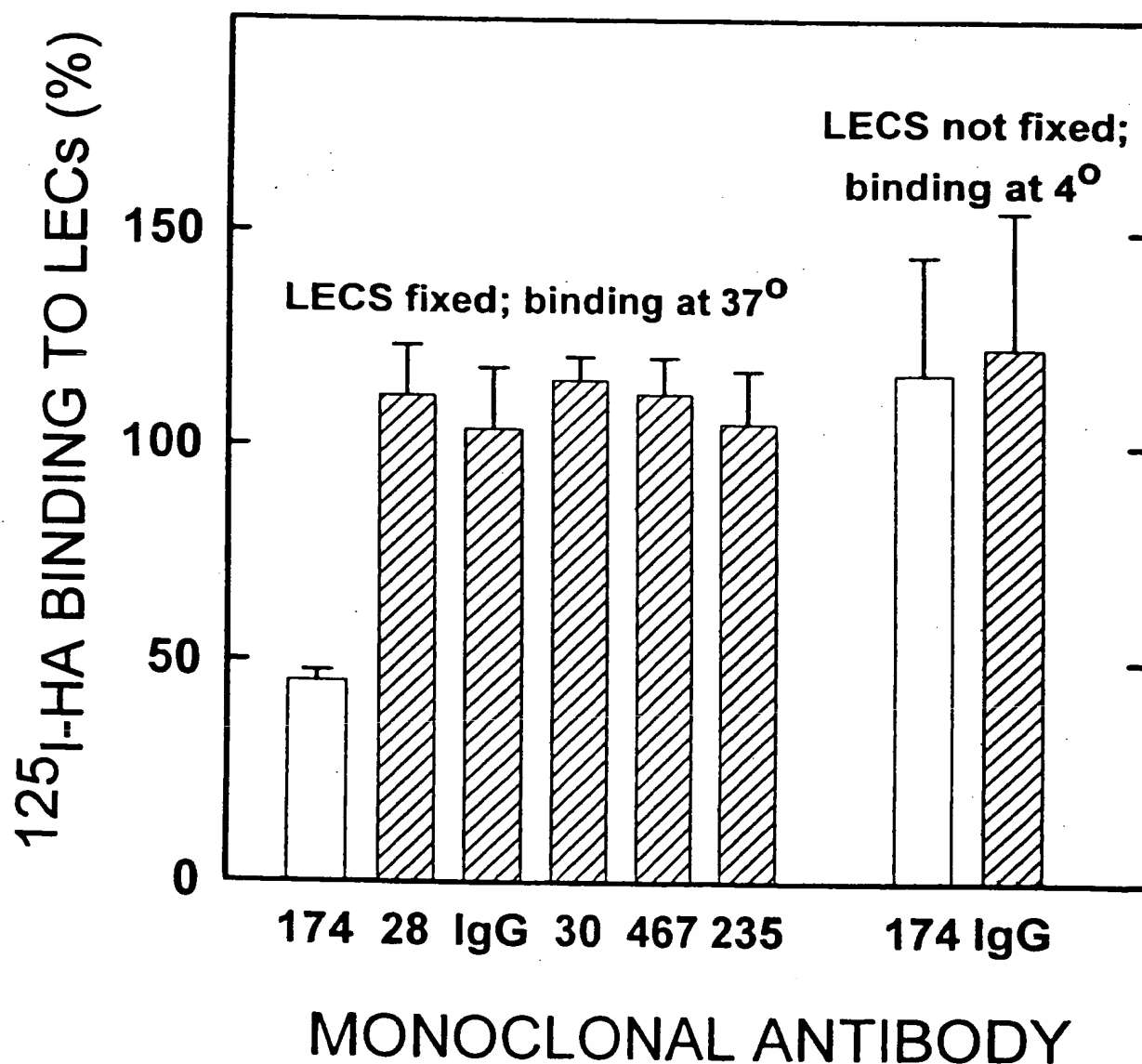
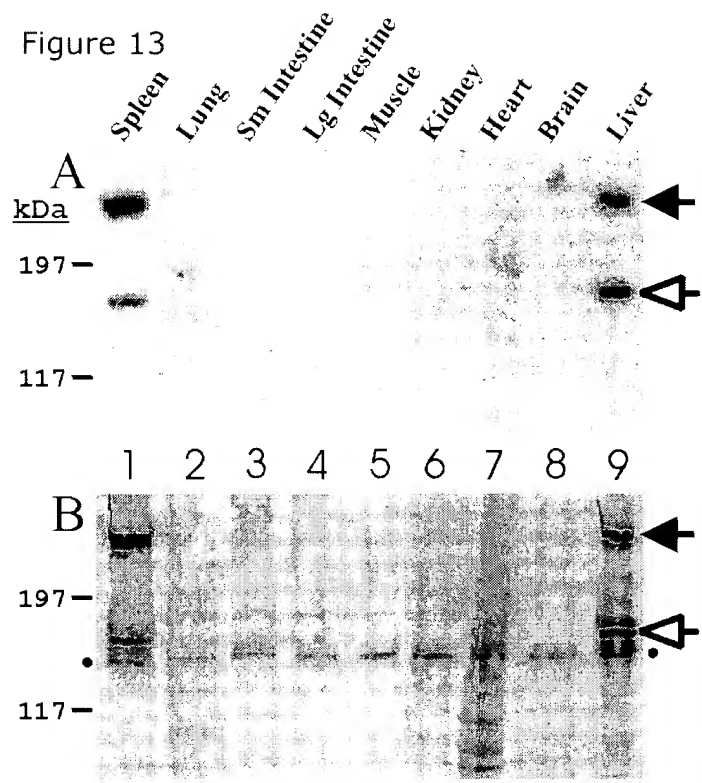


Figure 13





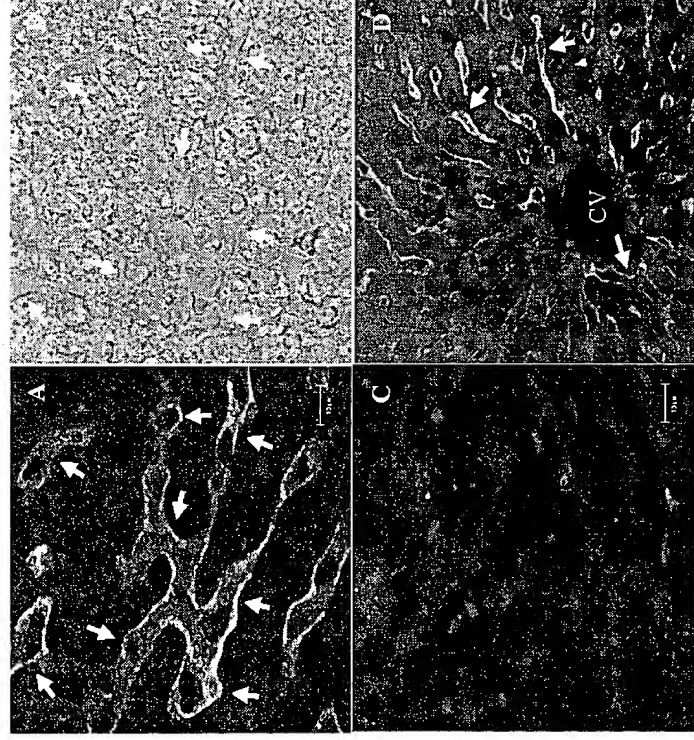


Figure 14

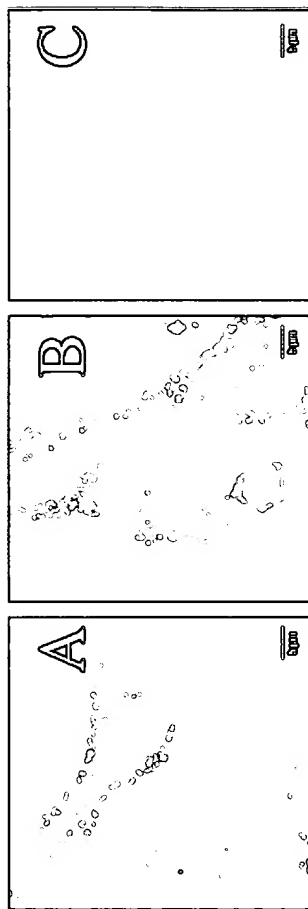


Figure 15

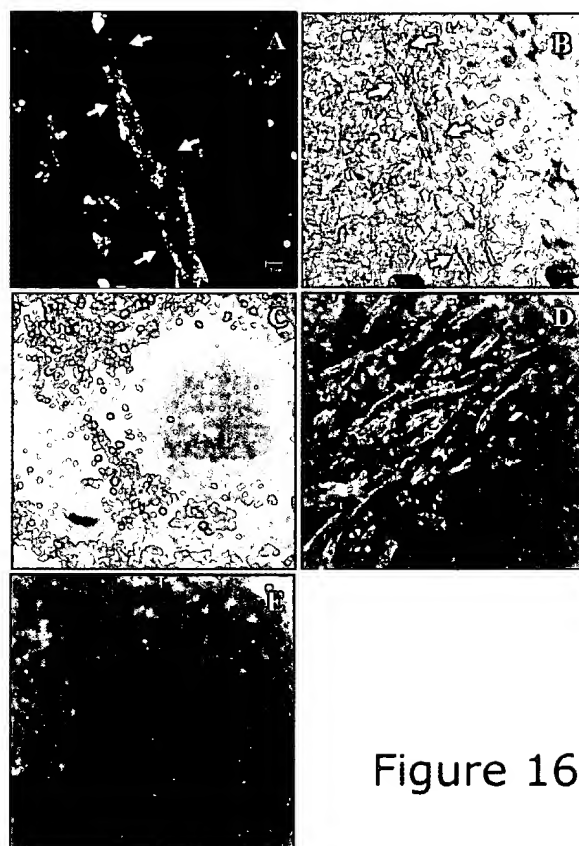


Figure 16

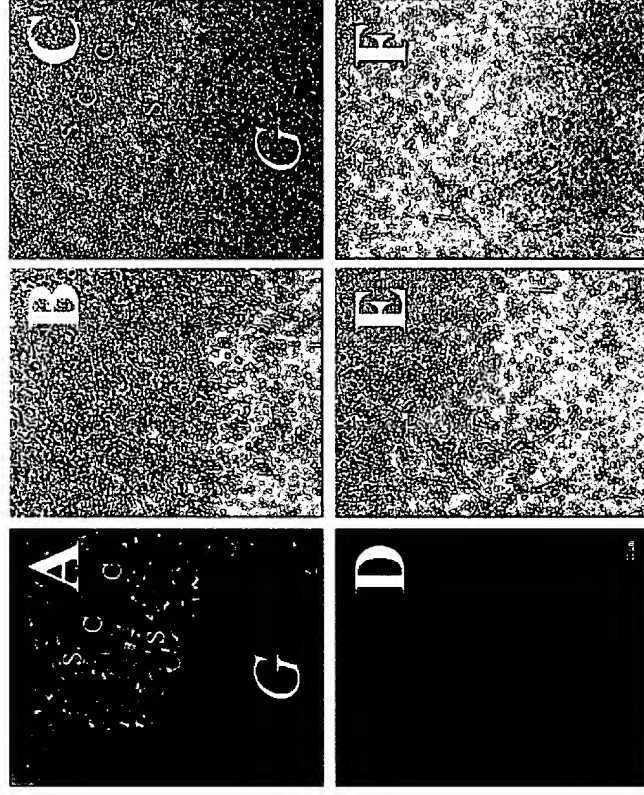
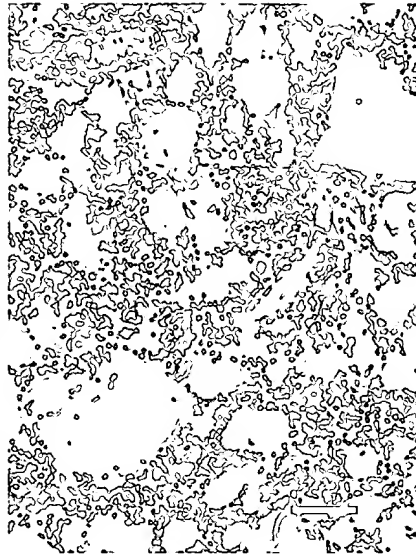
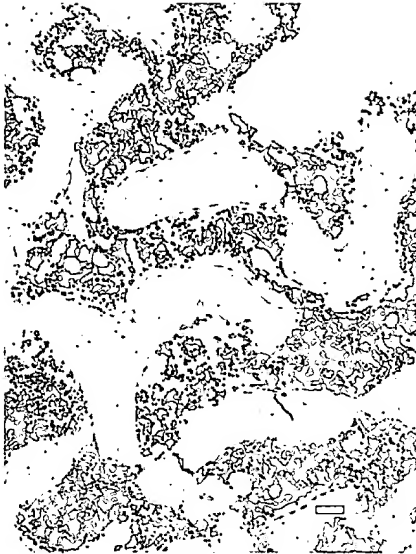


Figure 17

Figure 18

Immunolocalization of HARE  
in Bone Marrow

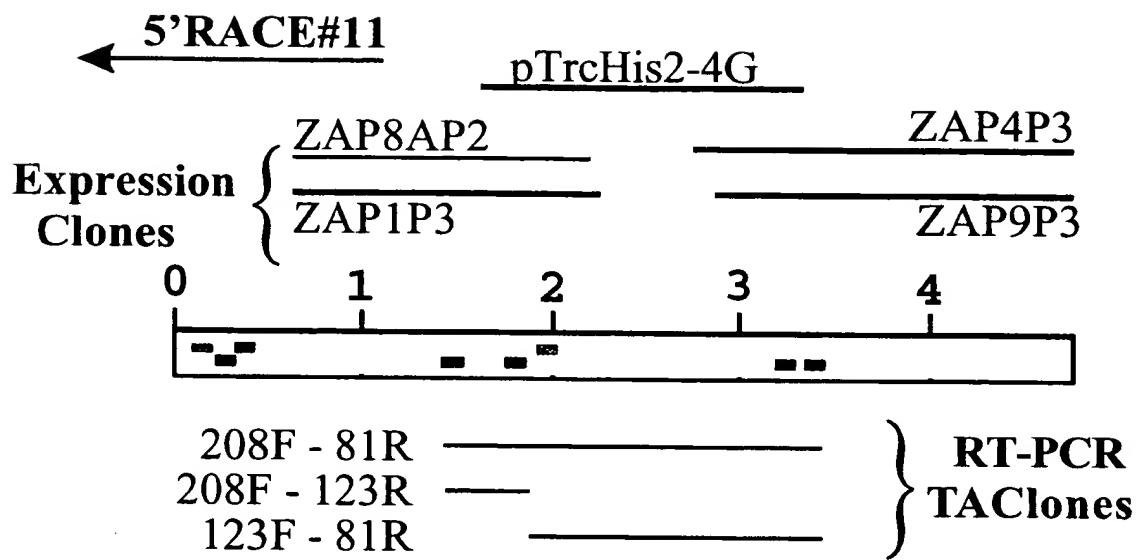
Control



Bars = 50  $\mu$ m

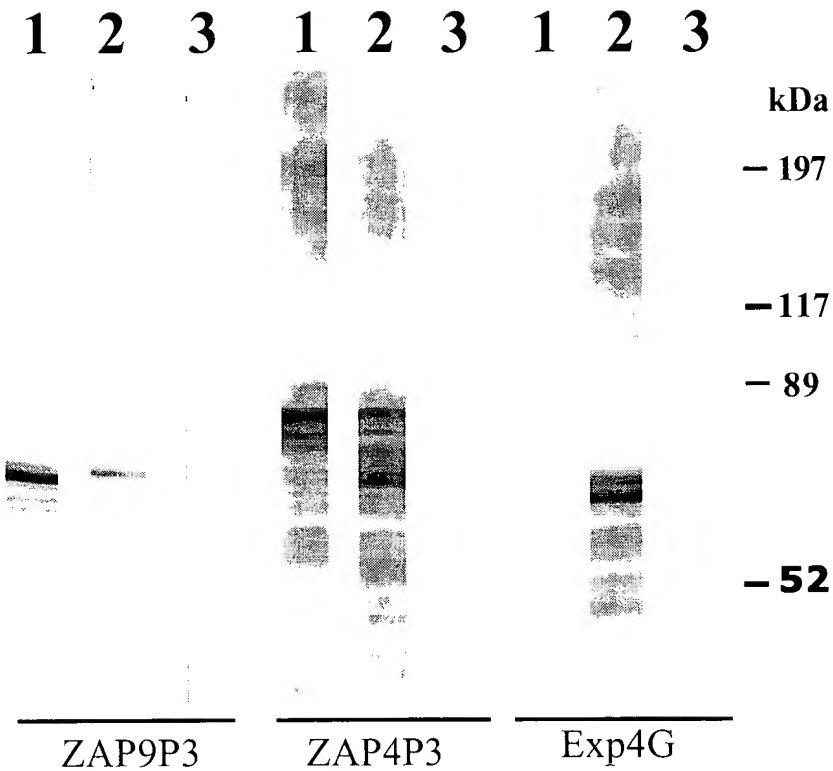
FO5240" 0E624860

Figure 19



09842930-042501

Figure 20



1 TCTTTACCAAGTCTACTCACCCGCTGTGGAGCAGATGCCACGACTTTCATTTCCTCCAGGTTACATTATTTACAACCTGGCAAGTGCAATCGAGTTCGCAGATGCTTATACGTGTTC  
1 S L P S L L T R L E A Q M P D Y T S I F F R G G Y I I H Y N L A S A I E S A D A Y T V F P

121 GTGCCAAACAATGAAGCCATCGAAAACCTATATCAGGGAAGAAGGCCACATCTCTAAAGGAAGATATTTCTACGGTACCATGTGGTCTGGGGGAAAGCTCCTGAAGAATGACTGTGCAT  
41 V P N N E A I E N Y I R E R A K A A T S L K E D I L R Y H V V L G E K L L K N D L H

241 AACGGCATGCACCGAGAGACCATGTGGGGTCTCTACCTCCTTGCCTTCTTCTCCGCAATGACCAGCTGTATGTAAATGAAGCTCCAATAAACTACACCAATGTGGCCACTGATAAA  
81 N G M H R E T M L G F S Y L L A F L R N D Q L Y V N E A P I N Y T N V A T D K

361 GGAGTGCATCTGGTCTGGAGAAAGTCTCGAAATTCAGAAAGACAGATGTGACAAATGACACCATTAATGTGAGAGGGAGTGTGGAAGTGTCCGCAAGCCCTCGCCACTC  
121 G V I H G L E K V L E I Q K N R C D N N D T I I F M G G A K R S V F I G C C Q P Q C T V R T I I T R A C

481 GAGACAAAACCATCTAGAGAGACGAGGAATGCATCTATCTACTCTACCTGAGGGAAGAGATCCGTATTACCTGGGTCCAGCCAGTGTGTGAGAACCATTTACAAGAGCCTGTC  
161 E T K P L R E T R K C I Y S I Y F C M G A K R S V F I G C C Q P Q C T V R T I I T R A C

601 TGGCTGGCTTCTTTGGCCCAAAATGCCAAGCCTGCCCGGGAGAGGTCAAATGTGTGCTCTGGGAACGGCTTCTGTCTGGGACGGTGTGAATGGCACTGGCACGTGCCAGTGCGGGTG  
201 W L A S L A H N A K P A P G E V K M C A L G T A S V W D G V N G T G T C Q C G L

721 GGCTTCATGGGACGCTGTGAACACTGCCTGACCTGGGGAAGTATGGTATCCACTGCACCAAGCATGCTCTGTGTCCATGGGAGATGTAGCCAAGGACCTTGGGAGACGGCTCTCG  
241 G F N G T A C E T C T E G K Y G I H C D Q A C S T G V H G R C S Q A G G P L D G G S C

841 GACTGTGACGTGGCTGGCGAGGAGTGAAGTGTGACATGGAGATCACCACAGACAACTGCAACGGGACCTGTACACCACTGCAACTGCCTTCTGGATCGACAGCGCAAAGCCTCGTGC  
281 D C D V G W R G V K C C D M E I T T D N C N G T C H T S A N C L L D P D G K A S C

961 AAATGTGCGGCAGGATTCGAGGGGAATGKACCGTGTGCACAGCCATCAATGCCTGTGAGACCAAGTGGAGGATGTTTACAAAGGCCGACTGTAAAAGAACCCAGGAAACCGG  
321 K C A A G F R G N G T V C T A I N A C E T S N G G C S T T K A D C K R T T P G N R

1081 GTGTGTGTGTGCAAGGCAGGCTATACCGCGCAGGCATCGTGTGCCTTGAATCAACCCGTGTTTGGAGAACCATGGTGGCTGTGACAGAAATGAGAGTGCACACAGACAGGGCCCAAC  
361 V C V C K A G Y T T G D G A L E I N P C L E N H G C C D R N A E C T T Q T G P N

1201 CAGGCGCTCTGTAATGCTTGTGCCGAAGTACTGGAGATGGAAGAGTCTGCTCGCTTATCAATGTCTGCTTAACGAACATGGCGGTCCAGTCCATTGCTTGTGCACTACACTGAG  
401 Q A V C C N C L P K Y T G D G K V C S L I N V C L T A C N N G G C S P F A F C N Y T E

1321 CAAGATCAAAGCATATGTACTCTCAAGCCAGCTACCGGGTGATGGAAATCGTCTGCGCGGCGAGCATCTACGGGAGCTTCCCAAGAACCCCTCGACGTCCCACTTCTTCCAGT  
441 Q D Q R I C T C K P D Y T G D G I V C R G S I Y G E L P K N P S T S Q Y F A T T C T G L

1441 CAGGAGCATGTGTCCGAGAGCTTGTGTGACCTGGCCCTTACCCTGTTCGCGCTTGTCTAGCTCTCTCAATCATGAGCCCGGATTAAAGACTGGGATCAGCAGGGCCTCATGTCC  
481 Q E H A V R E L A G P G P F T V F A P L S S S F N H E P R I K D W D Q Q G L M S

1561 CAGGTTCTTCGCTATCAGTGGTGGGCTGGCAGCAGTCTGTGTGGACAACCTAAAAGTGACCACAAGTGCCTACCATGACCCCTCAAGGAGGCCAGTGTTCATCTCTGTCTCTCAGGACACT  
521 Q V L R Y H V V G C Q Q L L D D N L K V T T S A T T L Q G A G E P V S I S V S Q D T

1681 GTGTTCATAAAACATGAGGCGAAGTCTGTCCAGTGACATCTCAGCACAATGGCGTATCCACGTTATAGACAAGTGTGTCTCTCCAAAACCTTGCTTATCACCCCAAGATGCC  
561 V F I N N E A K V C L S S D I I S T G N G V I H V I D K L L S P K N L L I T P K D A

1801 TTGGCAGGGTCTGCAAAATCTTACTACGTGGCAGCAAAACCGGATATACAAATGACAAAGTGTATCAGGACTCAGGCTGTGTCAGTATCATGACTCATTCACCAACCCCA  
601 L G R V L Q N L T T V A A N H G Y T K F S K L I Q D S G L L S V I T D S I H T P

1921 GTCACTGTCTTCTGGGCTACGGAACAAGCCGGAAGCTTGGCCCGCAGCAGCAGGACTTCTGTTCAATCAAGACAACAGGACAAGTCAAGTCTTACCTGAAGTTCACCGTGTAT  
641 V T V W P T D K A L E A L P P E Q Q D F L F N Q D N K D K L K S Y L K F H V I

2041 CGAGACTCCAAGGCTTTAGCTTCAGACCTCCCCAGGTCTGCTTCTGGAAGACCTGCAAGGCTCAGAGCTGAGTGTGAGGTGTGGAATGGCAGTGACATCGGTGAGCTCTTCTAAAC  
681 R D S K A L A S D L P R S A S W K T L Q G S E L S V R C C G T G S D I G E L F L N

2161 GAACAAATGTGCAGATTCATACACCGGGACTTGTGTTGACGTGGGTGTGGCTATGGCATGTACTGCCTACTCATGAATCCTACCTAGGTGGCCGATGTGACACTTTTACTCTCT  
721 E Q M C R F I H R G L L F D V G V A Y G I D C T L M N P T L G G R C D T F T T F

2281 GATATTCGGGGGAGTGCAGGAATGTGATTTTCACTCCCAAATGCCACTGAAGAGCAAGCAAAGGGCGTGAAGAAGAAGTGTATCTACAACCCGTTACCTTTTCAAGAGGAACGTGGAA  
761 D I P G E C G S C I F T P K C P L K S K P K G V K K K C I Y N P L P F R R N V E

2401 GGCTGCCAAGCCTGTGACCGTGGTATCAAACCCCGAGTGTGCGATGGTTACTTCATGCGAGCTGCGCTGGAGGACAGATACACCGTGTAAACACCGGGCATG  
801 G C Q N L C T V V I Q T P R C C H G Y F M P D C Q A C P G G P D T P C N N R G M

2521 TGCCCGCATCTGTACACACCCATGGGACGCTGCCTATGCCACACCGGCTTCAACGGGACACCTCGAGCTTCTGTCGTCGGAGATTTGGGCTGTAGTGTGACGCCCGCAGCTGTCTCC  
841 C R D L Y T P M G C Q L C H T G F N G T A C E L C W H G R F G P D C Q P R S C S

2641 GAGCATGGACAGTGTGATGAGGGATCACAGGCTCCGGGAGTGCTCTGTGAAACAGGGTGGACAGCGCTCTGTGTGACACTCCACAGCTGTATTGCGAGTGTGCACACCTGCTTGC  
881 E H G Q C D E G I T G S G E C L C E T G W T A A S C D T P T A V F A V C T P A C

2761 TCCGTGCACGCCACCTGTACGGAGAACAACGCTGTGTGTGTAATCGAAGGTGACGGGATCATGTCAGCTCGTGGACTTGTGAAACAGAAACAACCGGGGCTGTGCGAAG  
921 S V H A C T C T E N N T T C V C N L N Y E G D G I T C T V V D F C K A Q N N G G C A K

2881 GTCCGTAAAGTGTCCAGAAAGGCCAACGCTCTTTCAGCTGCAAGAAAGGCTACAAGGGGATGGTACAGCTGCATAGAGATACACCCCTGTGTCAGACGGTGTCAACGGGGATGC  
961 V A K C S Q K G T Q V S C S C K K G Y K G D G Y S C I E I D P C A D G V N G G C

3001 CATGACACCCACCTGCAGGATGACGGGCCAGCAAGCATAAGTGTGAATGTAAAGTCACTATGTCGGGACGGAGTGGACTGTGAGCTGAGCAGCTGCCGCTCGACCGTGTCTT  
1001 H E H A T C R M T G P G K H K C E C K S H Y V G D G V D C E P E Q L P L D R C L

3121 CAGGACAACGGACGTGCCACCCAGATGCCAGCTGTGACAGCTCTACTTCCAGGACACGACCTAGGATTCATCTACGCTCCCCCTGGGCGAGTACAACCTGACATTTGACAAA  
1041 Q D N G Q C C H P D A S C A D L T T Q D T T G V F H L R S P L G Q Y K L T F D K

3241 GCCAAGAAGCCTGTGCCAAGAAGCTGCGACCATAGCCACCTACAACAGCTCTCTATGCCCAAGGCAAGTATCACTGTGTCTGGCCGGCTGGCTGGAGAGTGGCGGGTGGCC  
1081 A K E A C A T I A T I T N Q Q L S Y A Q K A K Y H L C S A G W L E S G R V A

3361 TACCCGACTACGTATGCTCTCAGAAGTGTGGTGCAACGTTGTTGGGATCGTAGACTCGGATCGGAGGCAACAGAGTGAATGTGGGATGTCTTCTGTTACCGGATGAAAGATGTG  
1121 Y P T T Y A S Q K C G A N C V T V G I V D Y G C S R A N K S E M W D V F C Y R M K D V

3481 AACTGCACCTGCAAGGCAGGCTATGTGGGAGATGGCTTCTGTGACGTGGAACTCTGTGACGGTCTCATGTCTTCCCTCGCTCAAAACTTCTGACAGAGGTGCTGGCTTTTTC  
1161 N C T C K A G Y V G D G F S C S G C N L L Q V L M S F P S L T N F A L T E V L A F S

3601 AAGAGCTACGCCGAGGACAGGCACTTTTGAACACCTGACTGACCTGTGCATCCGTGGCACCTGTTTGGCAAGAACAGTGGGCTACCGGAAATGAAGACTGTCTGGCGGGAC  
1201 K S S A R G Q A F L K H L T D L S I R G T L F V P Q N S G L P G M K B L S G R D

3721 ATTGACACCACTACTAATGTCAACGTTCTCTTTACAATGACCTGTCAATGGTACCTTCTGAGGACTATGCTGGGAAGCAACTGCTTATCTTACCTCAGCAGGACAGCTCCAC  
1241 I E H H L T N V N V S F Y N D L V N G T F L R T M L G L L I T I T F S Q D Q L H

3841 CAAGAGACAGGTTTGTGGATGGAAGATCCATTCTGACGTGGGACATCATCGCCGCAATGGAATCCTCCATATTATTTCTGAACCTTTGAGAGCTCTCCACGGCAGCAACGGCTGCC  
1281 Q E T R F V D G R S I L Q W D I I A A N G I L H I I S E P L R A P P T A A T A A

3961 CACTCTGGCTGGGACAGGTATATCTGTGCCCTCGTCTGTGACGTGGTGCAGTGTCTGCGAGTACTCTTACTTCCGGCTAAAGCAGGAACCACTGGTTTCCAGCGTTTGTAT  
1321 H S G L G T G I F C A V V L V T G A I A L A A K Q R T T G A T T A F S D

4081 CAGAAGAGGACATTGATGTCTTGGCTTTGGCAAGCAGCAGCCCAAGAATATCGCAAAACCTCTGTATGAGACCTCAGCGCCGACCCCCAGAGTCTCTCTGTGACCCCTTACAGACC  
1361 Q K R T L M S W A S S S P R I S Q T L C M R P Q R R H P Q S P P V T P S Q T

4201 CTGGAACACAGGATCTGAGGACAGCACCTCTGGGGCACTCGGCTCTGACATGAGAAGCAAGCAACAGTACAGGTTCCACGGTTCACGGTTCACAGCCCCAGCTGT



Figure 22

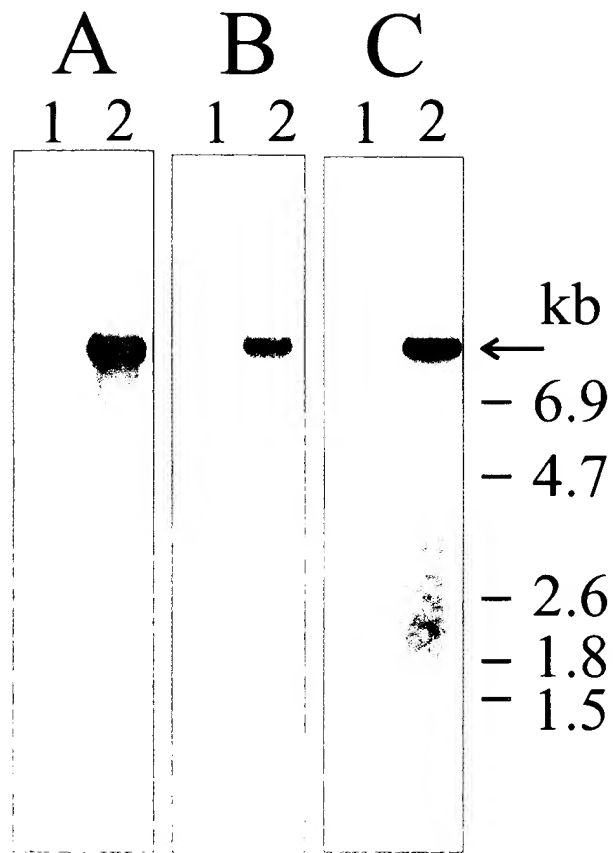
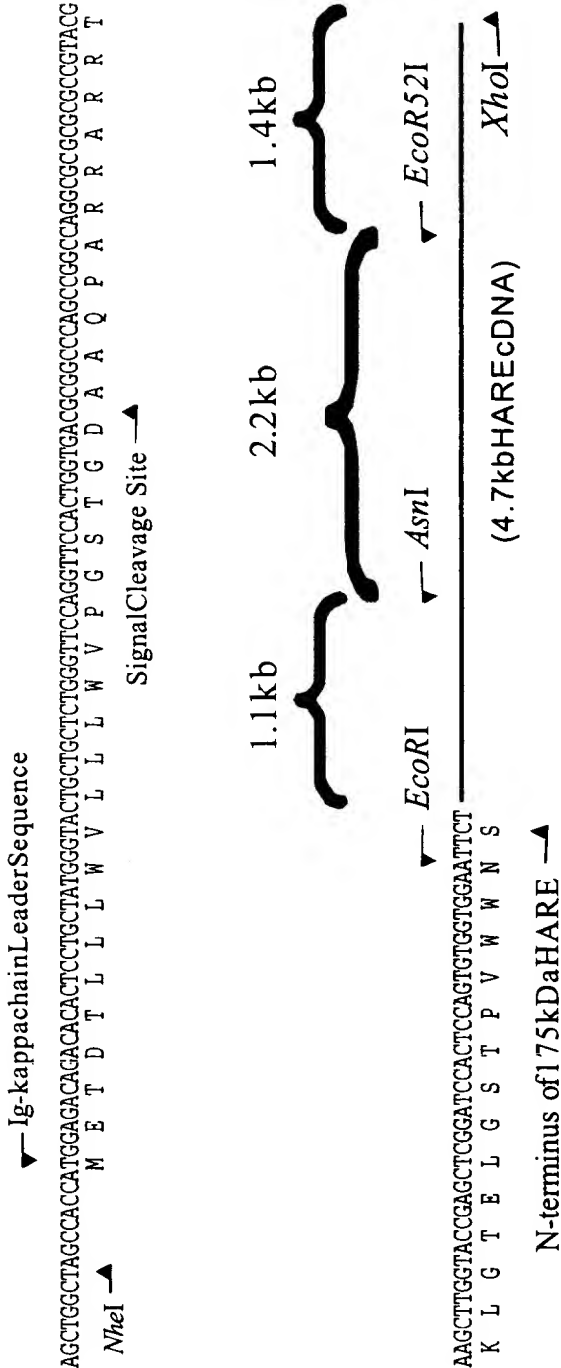


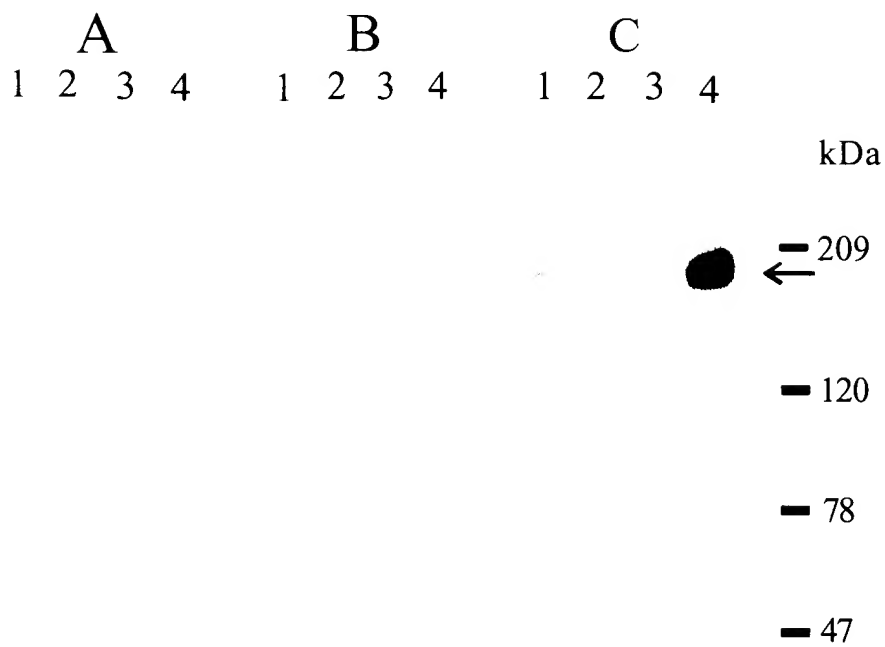


Figure 24



**Figure 25**

# Autoradiography



# Western Blot

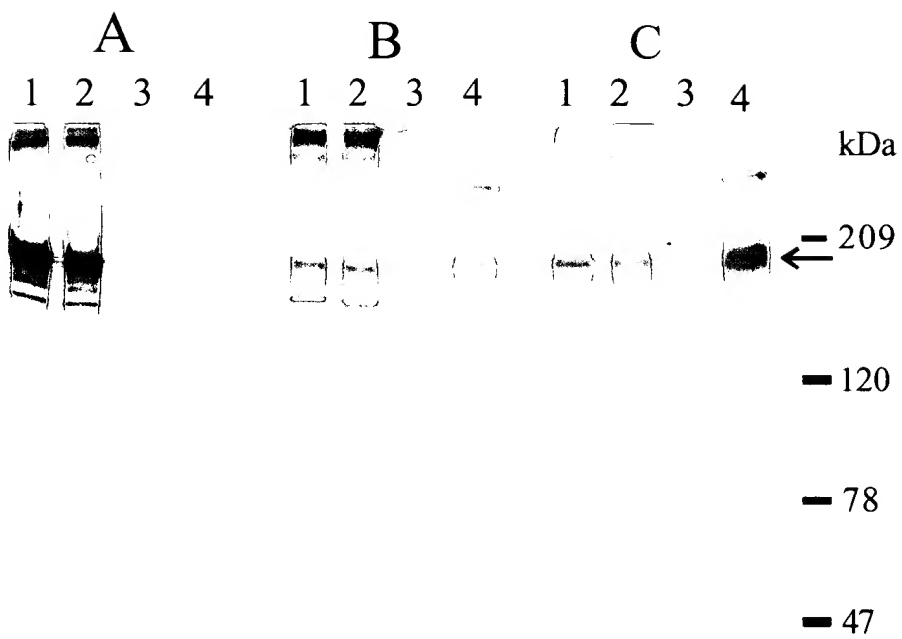
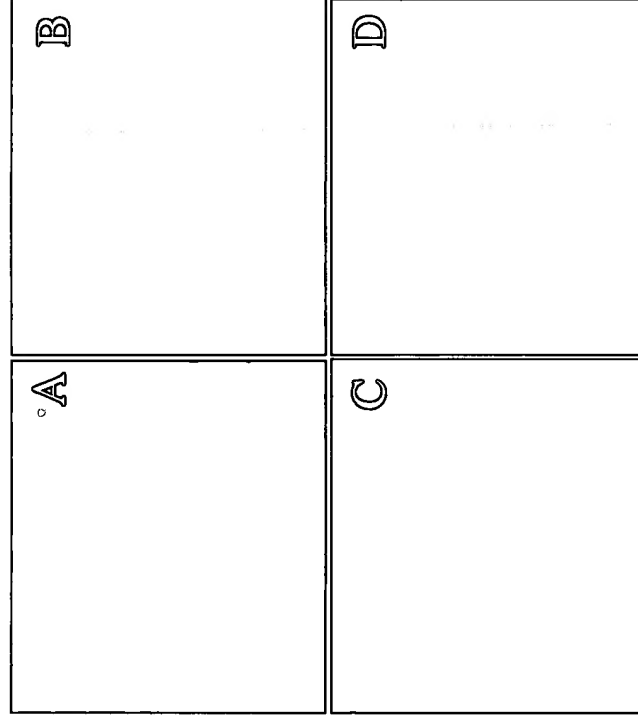


Figure 26



00524860

Figure 27A

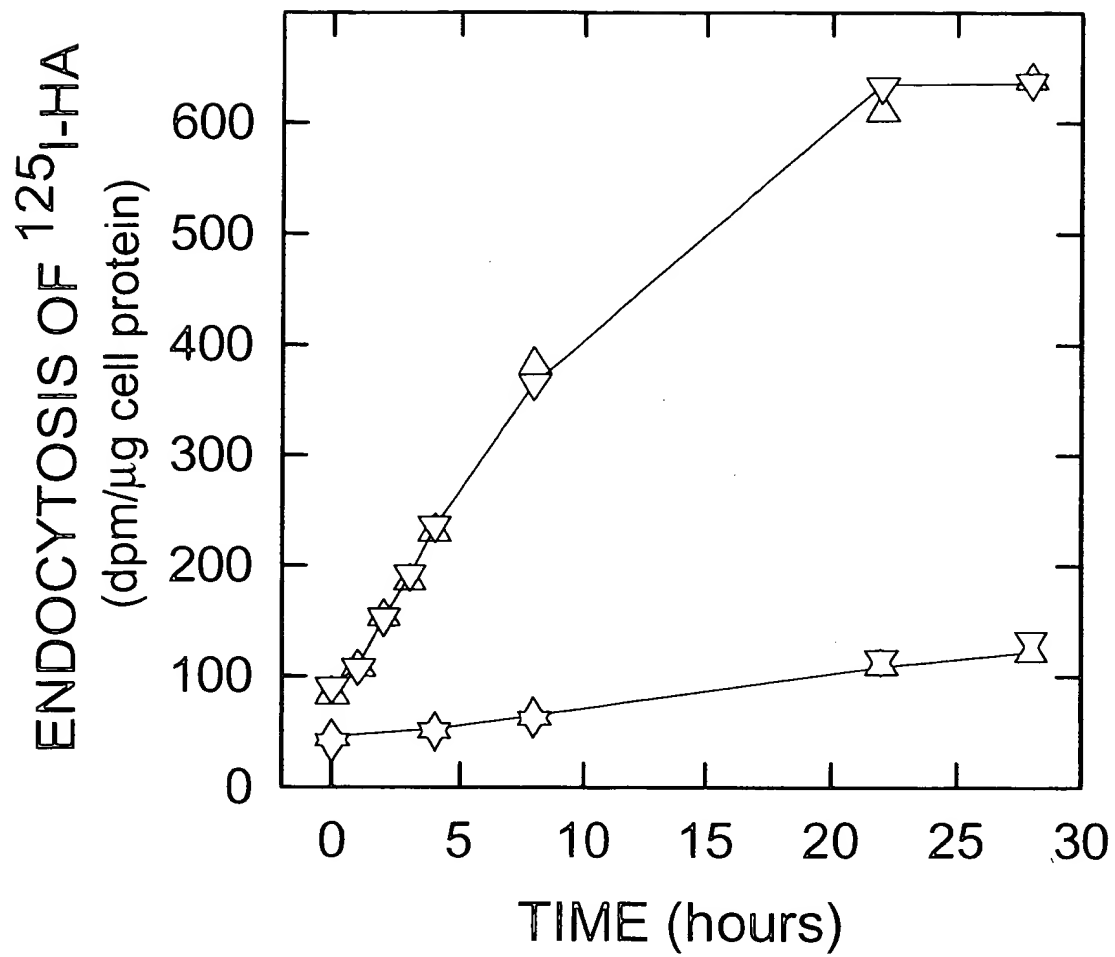


Figure 27B

**Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE**

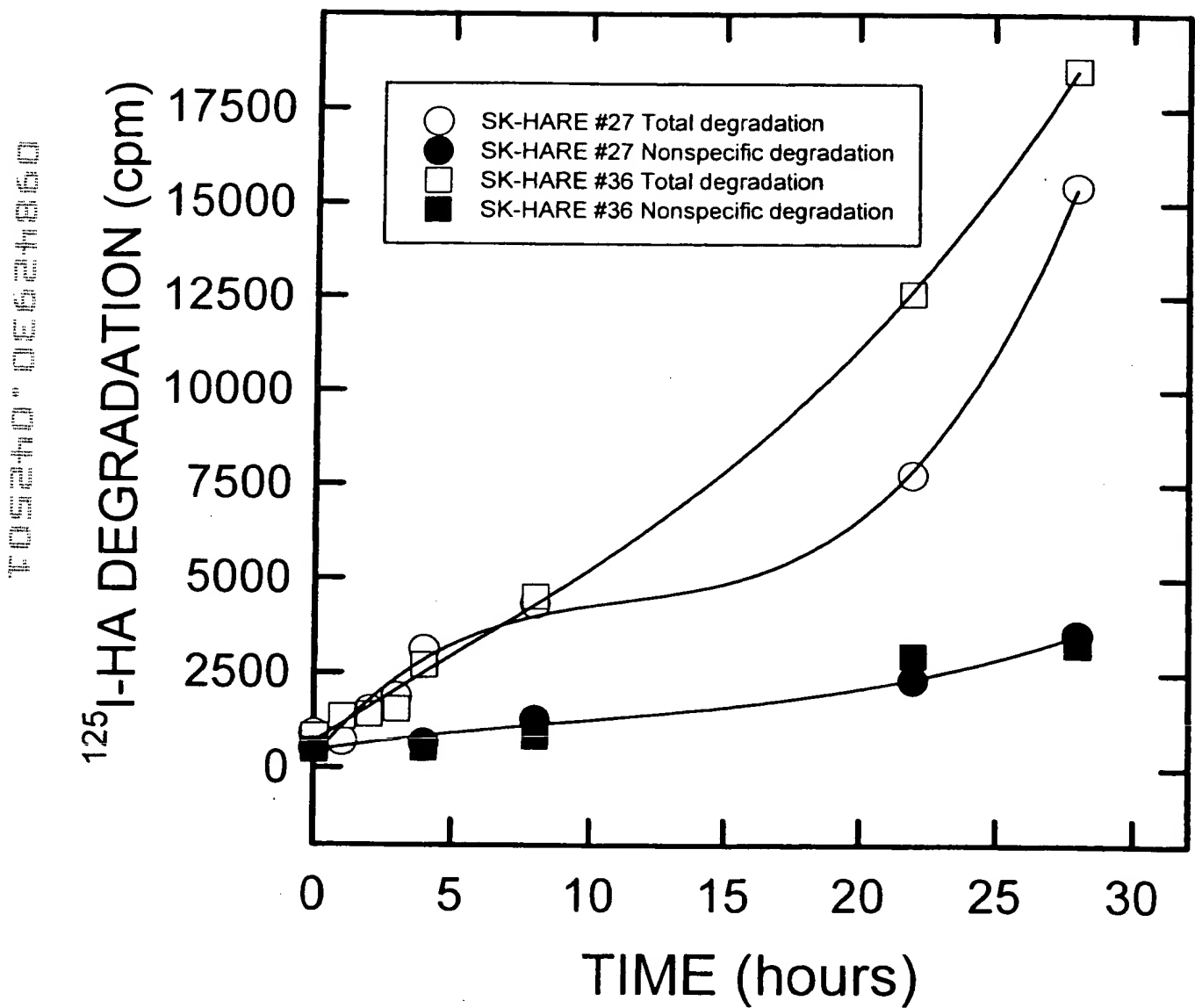


Figure 27C

# Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells

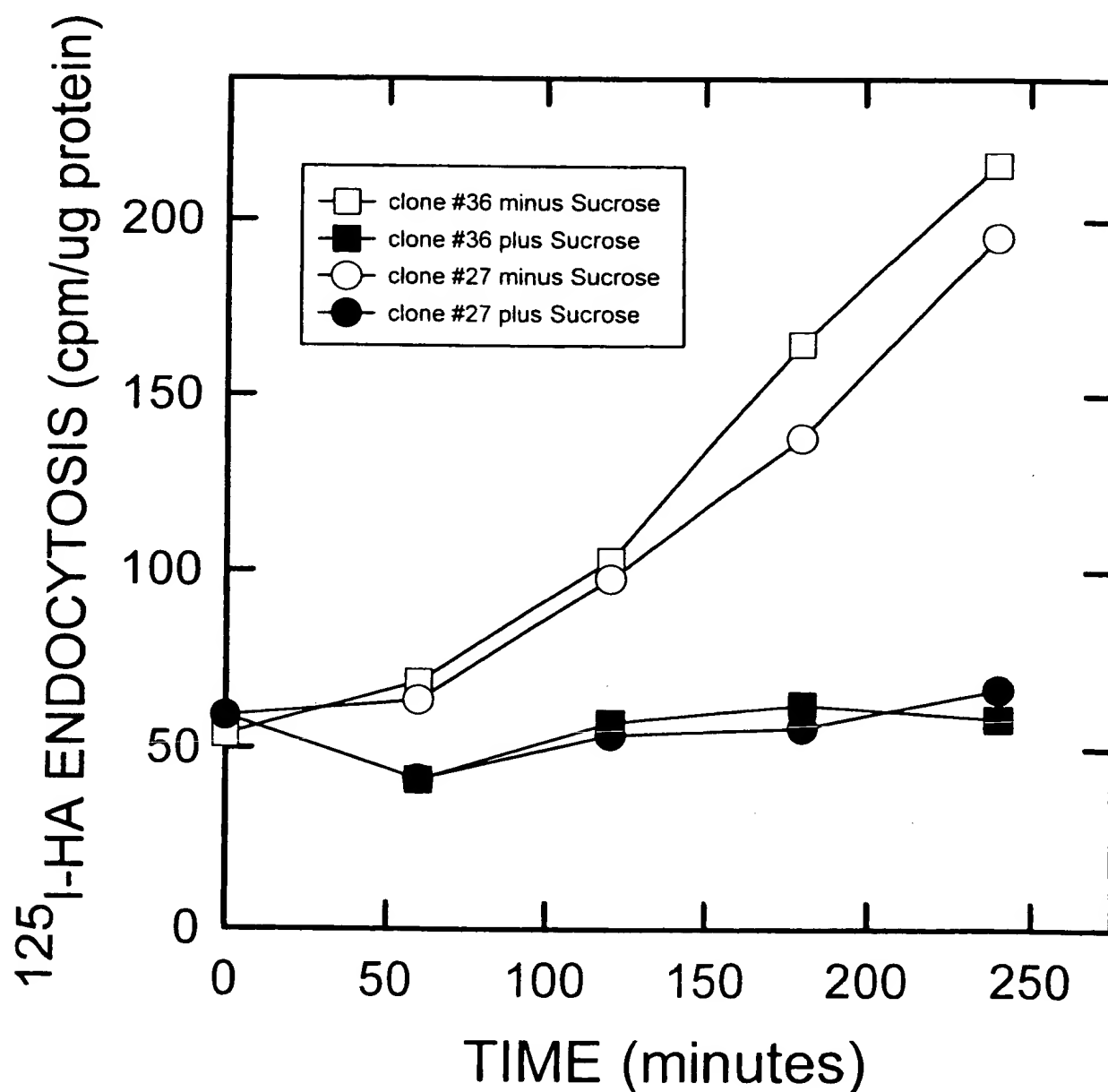
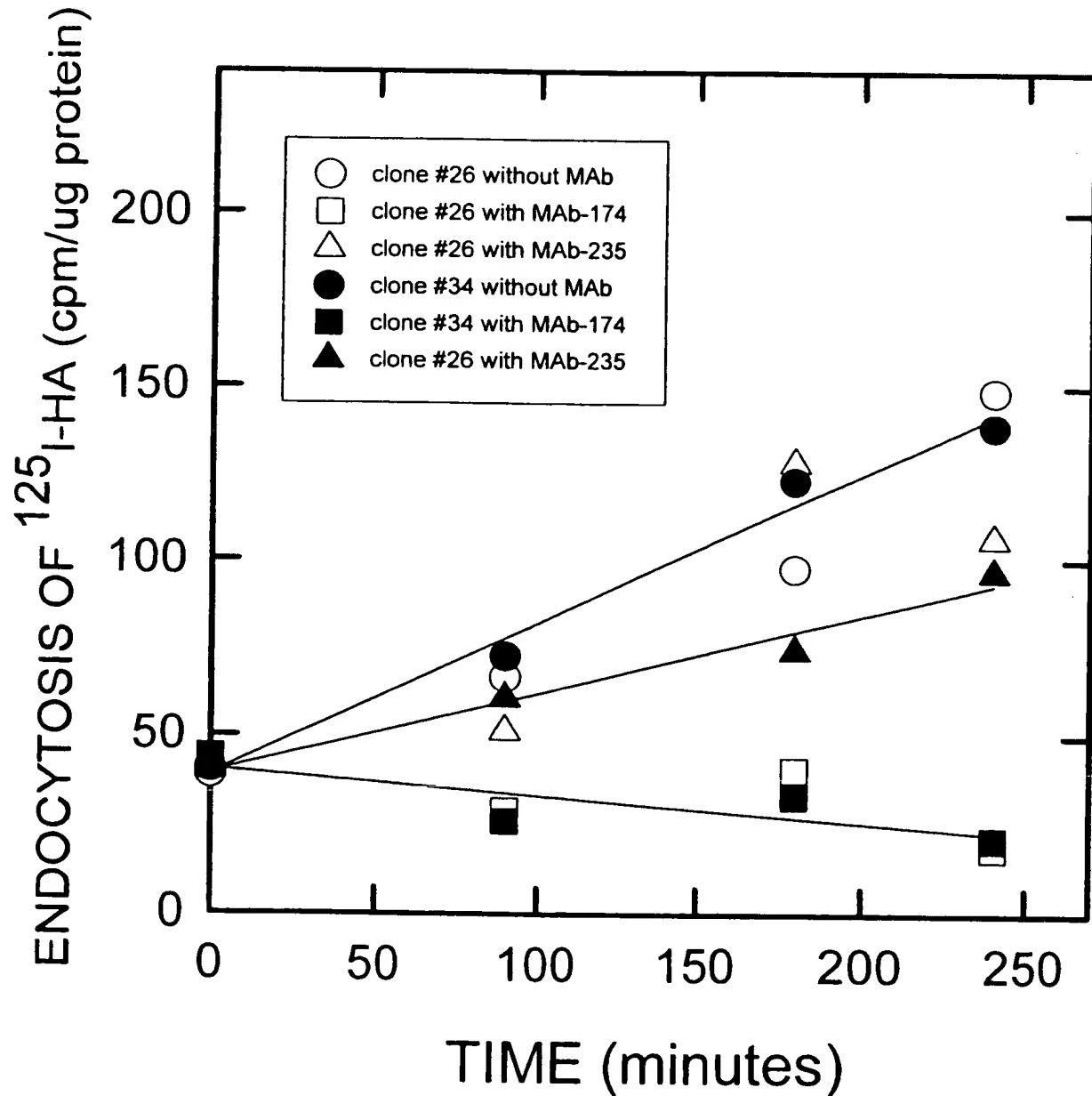




Figure 27D

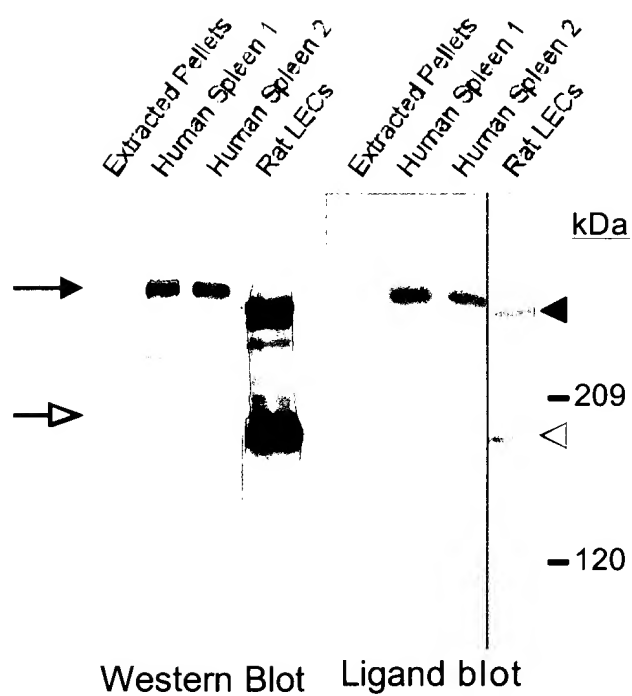
**Specific monoclonal antibodies against HARE  
inhibit HA endocytosis in SK-Hep1  
transfectants expressing the 175-kDa HARE**



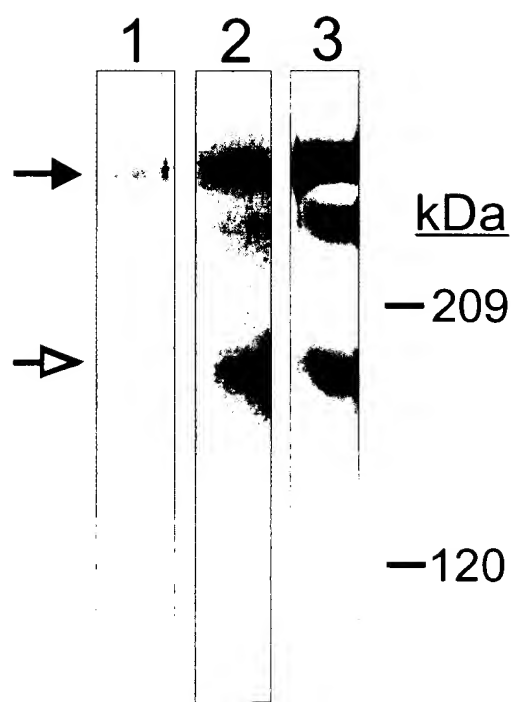
**Figure 28**

[illegible]

**Figure 29**



**Figure 3**



# Figure 31

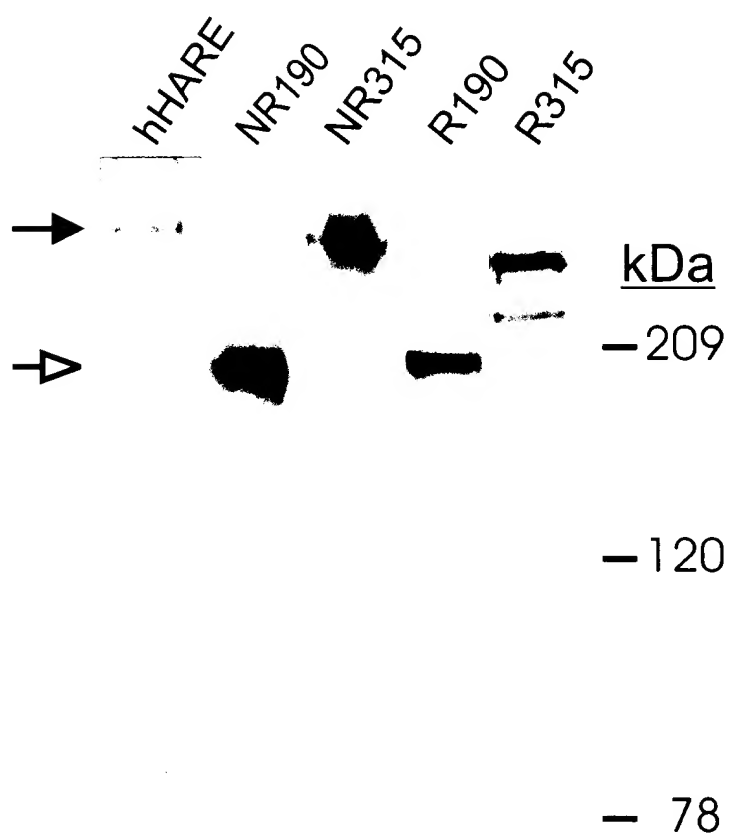
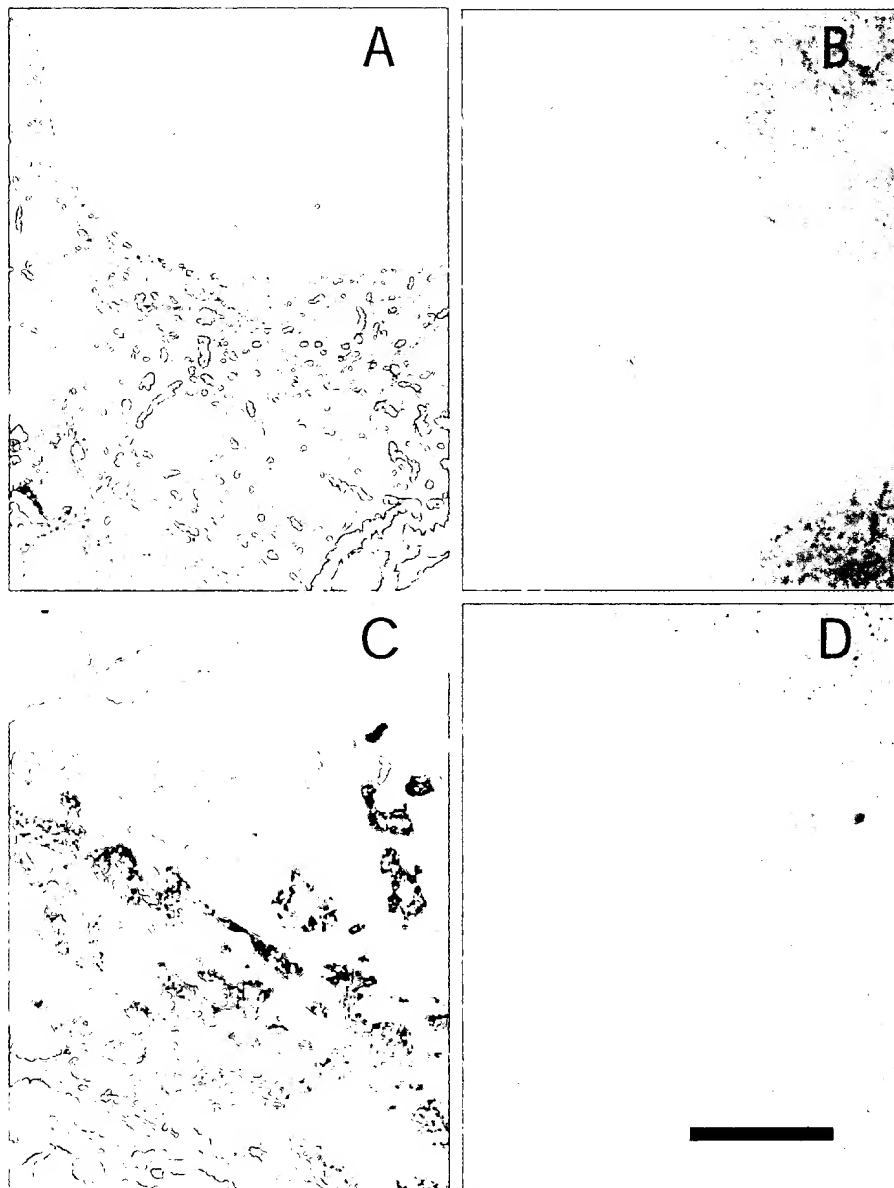
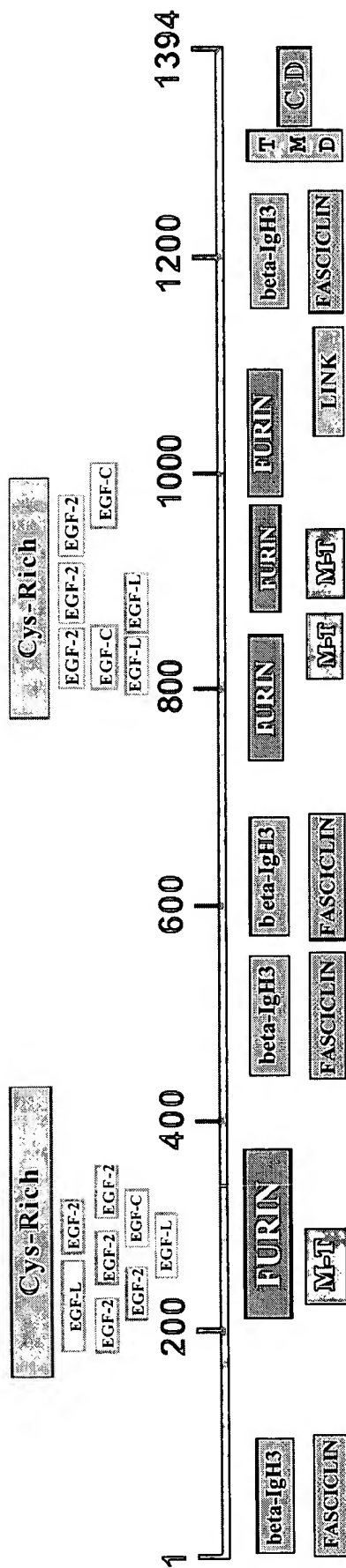


Figure 3 2



[illegible][illegible]

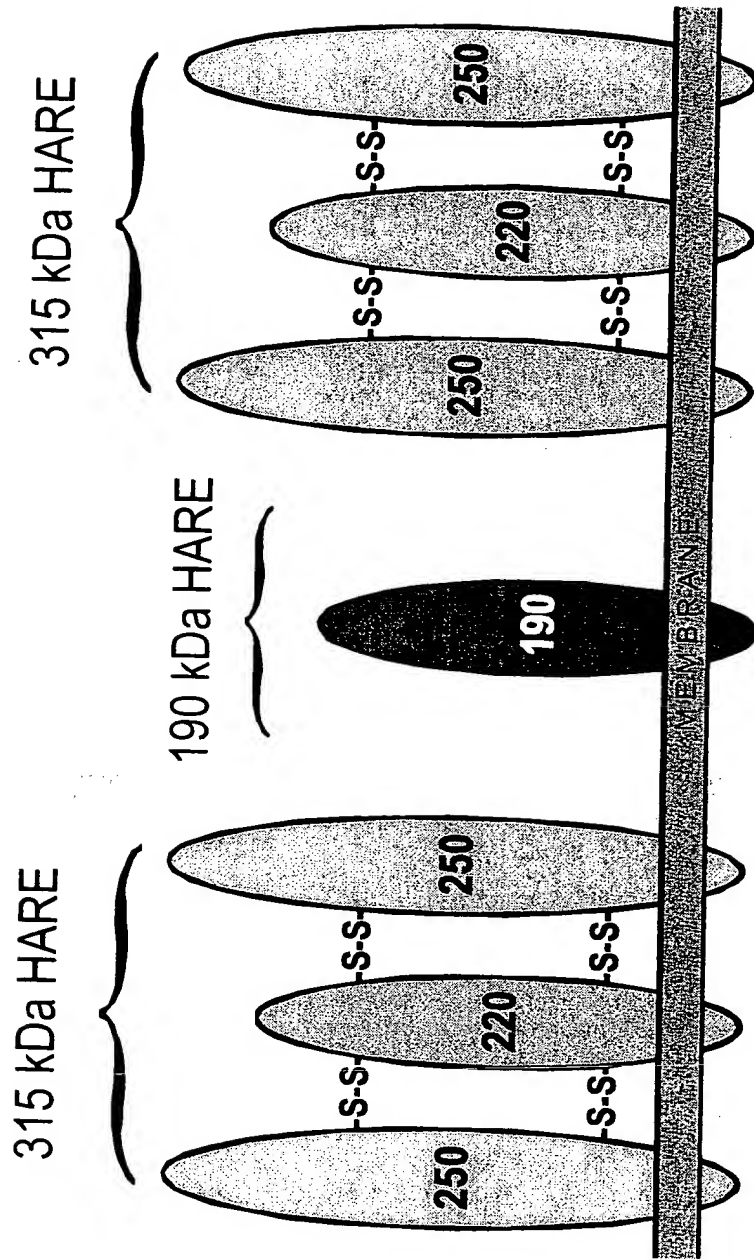
Figure 34





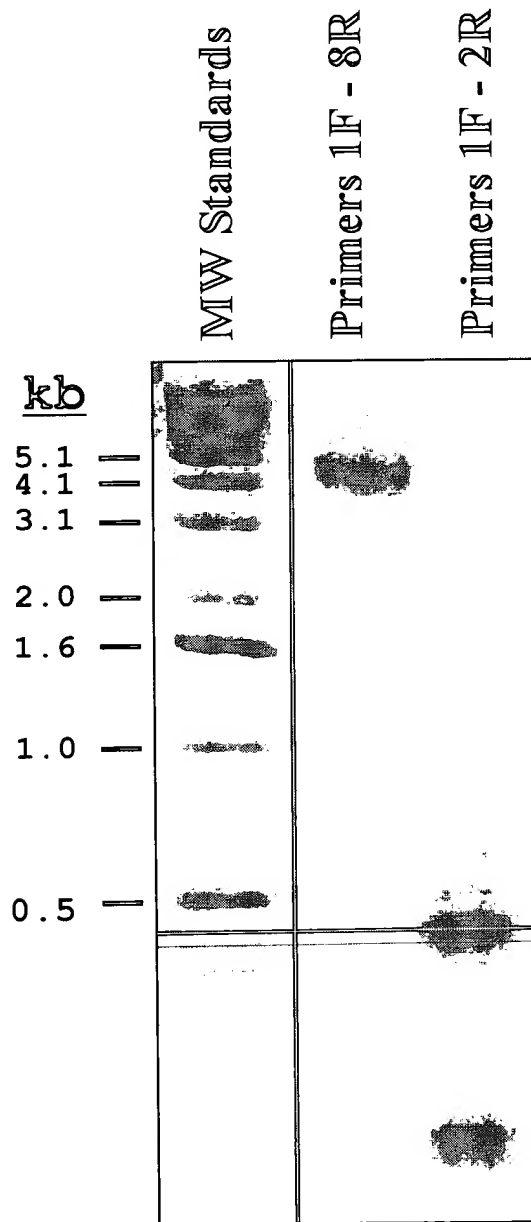
hHARE	1	IQYNLANAIEAADAYTVFAP	NNNAIENYIREKKVLSLEED	VLRYHVVLVEEKLKNDLHNG	MHRETMGLGFSYFLSFFLHND	QLYVNEAPIYTNVATDKGV
rHARE	23	IHYNLASAIESADAYTVFVP	NNEAIENYIREKKATSLKED	ILRYHVVLGEKLLKNDLHNG	MHRETMGLGFSYLLAFLRND	QLYVNEAPIYTNVATDKGV
hHARE	101	IHGKGVLEIQKWR	DNMDR	KSLGNEKRR	IYTSYFMGR	TLFIGQPKVRTVITRE
rHARE	123	IHGKGVLEIQKWR	DNMDR	IIVRGE	GK	SOQAP
hHARE	201	GNGICLDGVNGTGV	E	FGTA	ET	TEGKYGIH
rHARE	222	GTASVWDGVNGTGV	Q	GLG	ET	TEGKYGIH
hHARE	301	AAGFCGNGTGV	TAI	TAI	TAI	TAI
rHARE	322	AAGFCGNGTGV	TAI	TAI	TAI	TAI
hHARE	401	VLTNKG	SEFAL	NET	Q	VERT
rHARE	422	VLTNKG	SPFAL	NET	Q	DORI
hHARE	501	VLRYHVVA	HQLLLENLKI	SNATSLQGEPIVIVS	VSQSTV	YINNKAIISSDII
rHARE	522	VLRYHVVG	QQLLLDNLKVT	TSATTLQGEVPV	SISVSQD	FINNEAKVLS
hHARE	601	NLIQDSGLLSVITDPIHTPV	TLFWPTDQALHALPAEQQDF	LFNQDNKDKLKEYLKEHVIR	DAKVLAVDLPTSTAWKTLOG	SELSVK
rHARE	622	KLIQDSGLLSVITDPIHTPV	TVFWPTDKALEALPEEQQDF	LFNQDNKDKLKEYLKEHVIR	DAKVLAVDLPTSTAWKTLOG	SELSVK
hHARE	701	QTRIVQRELLFDLGVAVGI	D	LLIDPTLGR	DTFTTFD	ASGE
rHARE	722	QTRIVQRELLFDLGVAVGI	D	LLMNPTLGR	DTFTTFD	IPGE
hHARE	800	RDQA	PGGPDAP	NNRGV	LDQYSATGE	K
rHARE	822	PDQA	PGGPDTP	NNRGM	RDLYTPMGQ	L
hHARE	900	AHAT	KENNT	ET	NLDVEGD	GIT
rHARE	922	VHAT	TENNT	V	NLNVEGD	GIT
hHARE	1000	YVGDLN	EPEQLPIDR	LQ	DNGQ	HADAK
rHARE	1022	YVGDLN	EPEQLPLDR	LQ	DNGQ	HPDAS
hHARE	1100	PTAFASQ	SGVVGIVDYG	PRPKSEMWDVF	YRMKDVM	PRPKSEMWDVF
rHARE	1122	PTTYASQ	GANVVGIVDYG	SRANKSEMWDVF	YRMKDVM	SRANKSEMWDVF
hHARE	1200	LFVPQNSGLGENETLSGRDI	EHHLANVSMFFYNLDVNGT	EHHLANVSMFFYNLDVNGT	EHHLANVSMFFYNLDVNGT	EHHLANVSMFFYNLDVNGT
rHARE	1222	LFVPQNSGLPGNKSLSGRDI	EHHLTNVNVSFYNLDVNGT	EHHLTNVNVSFYNLDVNGT	EHHLTNVNVSFYNLDVNGT	EHHLTNVNVSFYNLDVNGT
hHARE	1300	HTGLGAGIFFAIIIVTGAVA	LAAYSIFRI	NRRRTIG	FOHFE	LAAYSIFRI
rHARE	1321	HSLGTGIFCAVVLVTGAIA	LAAYSIFRI	KORT	EGFORF	LAAYSIFRI
rHARE	1421	SQATTVTVP				

Figure 36



# Figure 37

Amplification of the 1394 amino acid HARE  
Open Reading Frame from a human lymph  
node cDNA Library



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## Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12  
(encoding 1357 of the 1394 amino acids disclosed here)

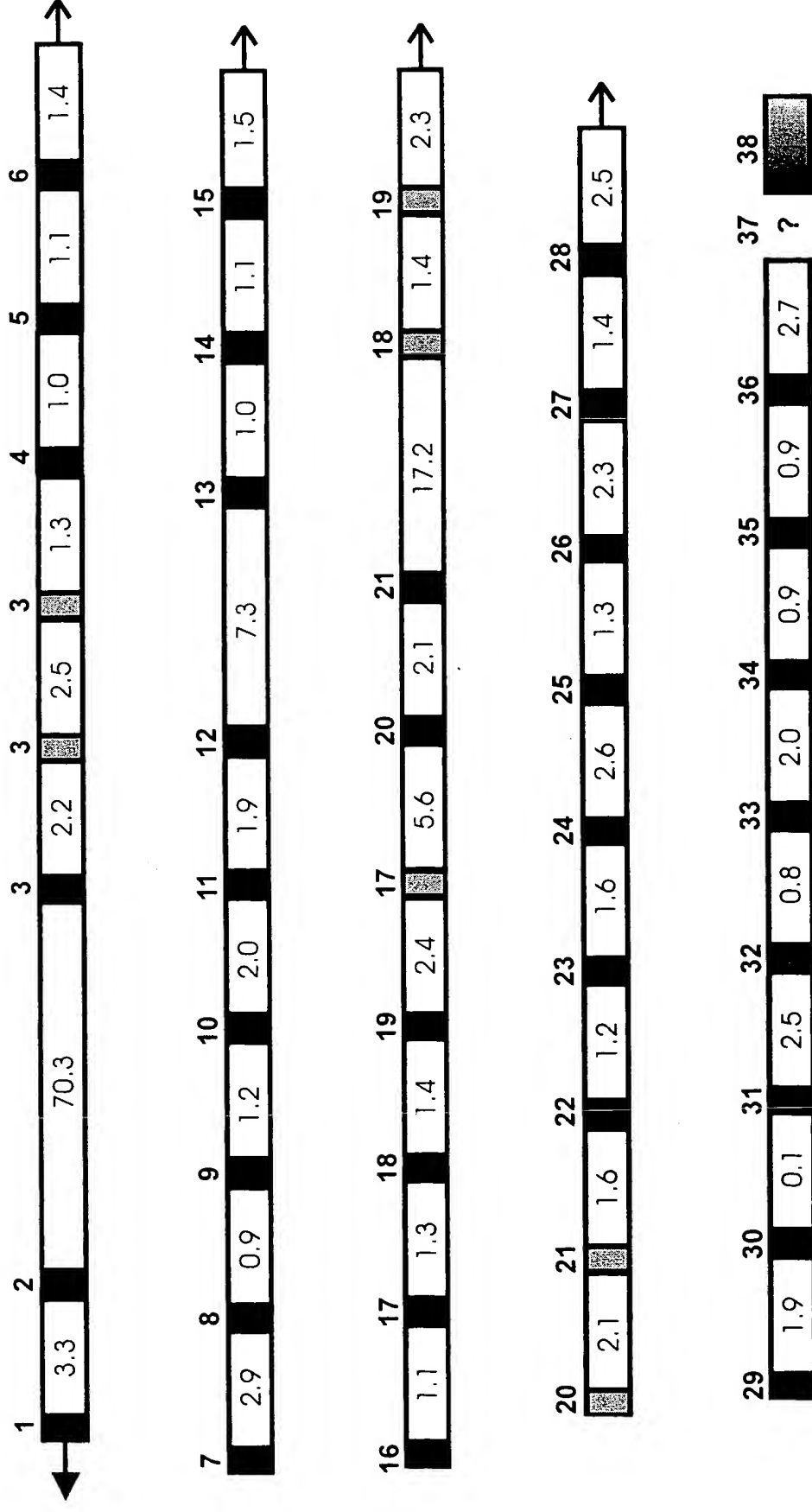


Figure 3 9

